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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/826,212

DATE: 04/19/2001

TIME: 12:21:58

Input Set : A:\seq list 1488 1280006.txt

Output Set: N:\CRF3\04192001\I826212.raw

5 <110> APPLICANT: Wei, Ying-Fei
7 Gentz, Reiner
9 Ruben, Steven
11 Ni, Jian
14 <120> TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
18 <130> FILE REFERENCE: 1488.1280006
C--> 22 <140> CURRENT APPLICATION NUMBER: US/09/826,212
C--> 22 <141> CURRENT FILING DATE: 2001-04-05
22 <160> NUMBER OF SEQ ID NOS: 26
26 <170> SOFTWARE: PatentIn version 3.0
30 <210> SEQ ID NO: 1
32 <211> LENGTH: 1392
34 <212> TYPE: DNA
36 <213> ORGANISM: Homo sapiens
40 <220> FEATURE:
42 <221> NAME/KEY: CDS
44 <222> LOCATION: (183)..(959)
48 <220> FEATURE:
50 <221> NAME/KEY: mat_peptide
52 <222> LOCATION: (261)..()
56 <220> FEATURE:
58 <221> NAME/KEY: sig_peptide
60 <222> LOCATION: (183)..(260)
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65 cctctccaag cgcacgaact cagccaacga tttctgatag atttttggga gtttgaccag 60
67 agatgcaagg ggtgaaggag cgcttcttac cgttagggaa ctctggggac agagcgcccc 120
69 ggccgcctga tggccgaggc aggtgtcgac ccaggaccca ggacggcgtc gggaaccata 180
71 cc atg gcc cgg atc ccc aag acc cta aag ttc gtc gtc gtc atc gtc 227
72 Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val
73 -25 -20 -15
75 gcg gtc ctg ctg cca gtc cta gct tac tct gcc acc act gcc cgg cag 275
76 Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln
77 -10 -5 -1 1 5
79 gag gaa gtt ccc cag cag aca gtg gcc cca cag caa cag agg cac agc 323
80 Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser
81 10 15 20
83 ttc aag ggg gag gag tgt cca gca gga tct cat aga tca gaa cat act 371
84 Phe Lys Gly Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr
85 25 30 35
87 gga gcc tgt aac ccg tgc aca gag ggt gtg gat tac acc aac gct tcc 419
88 Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser
89 40 45 50
91 aac aat gaa cct tct tgc ttc cca tgt aca gtt tgt aaa tca gat caa 467
92 Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
93 55 60 65
95 aaa cat aaa agt tcc tgc acc atg acc aga gac aca gtg tgt cag tgt 515
96 Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln Cys

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97 70          75          80          85
99 aaa gaa ggc acc ttc cgg aat gaa aac tcc cca gag atg tgc cgg aag      563
100 Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys Arg Lys
101          90          95          100
103 tgt agc agg tgc cct agt ggg gaa gtc caa gtc agt aat tgt acg tcc      611
104 Cys Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser
105          105          110          115
107 tgg gat gat atc cag tgt gtt gaa gaa ttt ggt gcc aat gcc act gtg      659
108 Trp Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val
109          120          125          130
111 gaa acc cca gct gct gaa gag aca atg aac acc agc ccg ggg act cct      707
112 Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro
113          135          140          145
115 gcc cca gct gct gaa gag aca atg aac acc agc cca ggg act cct gcc      755
116 Ala Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala
117 150          155          160          165
119 cca gct gct gaa gag aca atg acc acc agc ccg ggg act cct gcc cca      803
120 Pro Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro
121          170          175          180
123 gct gct gaa gag aca atg acc acc agc ccg ggg act cct gcc cca gct      851
124 Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala
125          185          190          195
127 gct gaa gag aca atg acc acc agc ccg ggg act cct gcc tct tct cat      899
128 Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His
129          200          205          210
131 tac ctc tca tgc acc atc gta ggg atc ata gtt cta att gtg ctt ctg      947
132 Tyr Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu
133          215          220          225
135 att gtg ttt gtt tgaaagactt cactgtggaa gaaattcctt ccttacctga      999
136 Ile Val Phe Val
137 230
139 aaggttcagg taggcgctgg ctgaggggcgg ggggcgctgg acactctctg ccctgcctcc      1059
141 ctctgctgtg ttccacaga cagaaacgcc tgcccctgcc ccaagtccctg gtgtctccag      1119
143 cctggctcta tcttcctcct tgtgatcgtc ccatcccccac atcccgtgca cccccagga      1179
145 ccctgggtctc atcagtcctt ctccctggagc tgggggtcca cacatctccc agccaagtcc      1239
147 aagaggcagg gccagttcct cccatcttca ggcccagcca ggcagggggc agtcggctcc      1299
149 tcaactgggt gacaagggtg aggatgagaa gtgggtcacgg gatttattca gccttgggtca      1359
151 gagcagaaca cagagatttt ccgtgaaaaa aaa      1392
154 <210> SEQ ID NO: 2
156 <211> LENGTH: 259
158 <212> TYPE: PRT
160 <213> ORGANISM: Homo sapiens
164 <400> SEQUENCE: 2
166 Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val Ala
167 -25 -20 -15
170 Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu
171 -10 -5 -1 1 5
174 Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe
175 10 15 20

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/826,212

DATE: 04/19/2001

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Input Set : A:\seq list 1488 1280006.txt

Output Set: N:\CRF3\04192001\I826212.raw

```

178 Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly
179      25      30      35
182 Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
183      40      45      50
186 Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
187 55      60      65      70
190 His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln Cys Lys
191      75      80      85
194 Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys Arg Lys Cys
195      90      95      100
198 Ser Arg Cys Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp
199     105     110     115
202 Asp Asp Ile Gln Cys Val Glu Phe Gly Ala Asn Ala Thr Val Glu
203     120     125     130
206 Thr Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala
207 135     140     145     150
210 Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro
211     155     160     165
214 Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala
215     170     175     180
218 Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
219     185     190     195
222 Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr
223     200     205     210
226 Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu Ile
227 215     220     225     230
230 Val Phe Val
234 <210> SEQ ID NO: 3
236 <211> LENGTH: 455
238 <212> TYPE: PRT
240 <213> ORGANISM: Homo sapiens
244 <400> SEQUENCE: 3
246 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
247 1      5      10      15
249 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
250     20     25     30
252 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
253     35     40     45
255 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
256     50     55     60
258 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
259 65     70     75     80
261 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
262     85     90     95
264 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
265    100    105    110
267 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
268    115    120    125
270 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe

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PATENT APPLICATION: US/09/826,212

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Input Set : A:\seq list 1488 1280006.txt

Output Set: N:\CRF3\04192001\I826212.raw

```

271      130      135      140
273 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
274 145      150      155      160
276 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
277      165      170      175
279 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
280      180      185      190
282 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
283      195      200      205
285 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
286      210      215      220
288 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
289 225      230      235      240
291 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
292      245      250      255
294 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
295      260      265      270
297 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
298      275      280      285
300 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
301      290      295      300
303 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
304 305      310      315      320
306 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
307      325      330      335
309 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
310      340      345      350
312 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
313      355      360      365
315 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
316      370      375      380
318 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
319 385      390      395      400
321 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
322      405      410      415
324 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
325      420      425      430
327 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
328      435      440      445
330 Pro Ala Pro Ser Leu Leu Arg
331      450      455
333 <210> SEQ ID NO: 4
335 <211> LENGTH: 461
337 <212> TYPE: PRT
339 <213> ORGANISM: Homo sapiens
343 <400> SEQUENCE: 4
345 Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
346 1      5      10      15
348 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr

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TIME: 12:21:58

Input Set : A:\seq list 1488 1280006.txt

Output Set: N:\CRF3\04192001\I826212.raw

```

349          20          25          30
351 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
352          35          40          45
354 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
355          50          55          60
357 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
358 65          70          75          80
360 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
361          85          90          95
363 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
364          100          105          110
366 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
367          115          120          125
369 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
370          130          135          140
372 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
373 145          150          155          160
375 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
376          165          170          175
378 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
379          180          185          190
381 Asn Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
382          195          200          205
384 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
385          210          215          220
387 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
388 225          230          235          240
390 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
391          245          250          255
393 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
394          260          265          270
396 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
397          275          280          285
399 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
400          290          295          300
402 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
403 305          310          315          320
405 Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
406          325          330          335
408 Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
409          340          345          350
411 Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
412          355          360          365
414 Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
415          370          375          380
417 Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
418 385          390          395          400
420 Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
421          405          410          415

```

Please Note:

Use of n and/ r Xaa have been detected in the Sequenc Listing. Please review the Sequence Listing t ensure that a corresp nding explanation is presented in the <220> to <223> fields of each sequence which presents at least ne n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/826,212

DATE: 04/19/2001

TIME: 12:21:59

Input Set : A:\seq list 1488 1280006.txt

Output Set: N:\CRF3\04192001\I826212.raw

L:22 M:270 C: Current Application Number differs, Replaced Current Application No
L:22 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1513 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1517 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1581 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1591 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1733 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:1849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1851 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1855 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18